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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/960,631A

DATE: 03/29/2002
TIME: 13:28:15

Input Set : A:\266_171.ST25.txt
Output Set: N:\CRF3\03292002\I960631A.raw

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 3 <110> APPLICANT: MIROCHNITCHENKO, Oleg
 4         WEI, Jiang
 5         INOUYE, Masayori
 7 <120> TITLE OF INVENTION: SOLUBLE ISCHEMIA ACTIVATED PROTEIN
 9 <130> FILE REFERENCE: 266/171
11 <140> CURRENT APPLICATION NUMBER: US 09/960,631A
12 <141> CURRENT FILING DATE: 2001-09-20
14 <150> PRIOR APPLICATION NUMBER: US 60/233,819
15 <151> PRIOR FILING DATE: 2000-09-20
17 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 840
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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29 agcgaggggc ctgctggctc ccggagcggt cgcctcttcc gcccgccgag tcccgctccg     120
31 gcggcccccg cgcccggct gttgcggctc ccggggagcg gggccgtgca ggccgcgagc      180
33 ccggagcgcg ccggctggac cgaggcgctg cgggccgccg tggccgagct cgcgcgccggc    240
35 gccgtggtgg ccgtccccac cgatacgctg tacggcctgg cctgcgcggc gagctgctcg     300
37 gcggctctgc gcgctgtgta ccgcctcaag ggtcgcagcg aggccaagcc tctggccgta     360
39 tgcctcggcc gcgtggccga cgtctacaga tactgccgtg tgagagtacc tgaggggctc     420
41 ctgaaagacc tactgccagg accagtgacc ctggtgatgg aacgctcgga ggagctcaac     480
43 aaggacctaa accctttac gcctcttgta ggcattcgga ttcctgatca tgcttttatg      540
45 caagacttgg ctcagatgtt tgagggtccg cttgctctca ctagtgccaa cctcagctcc     600
47 caggccagtt ctctgaatgt cgaggagttc caggatctct ggcctcagtt gtccttggtt     660
49 attgatgggg gacaaattgg ggatggccag agccccgagt gtcgccttgg ctcaactgtg     720
51 gttgatttgt ctgtgcccgg aaagtttggc atcattcgtc caggctgtgc cctggaaagt     780
53 actacagcca tcctccaaca gaagtacgga ctgctcccct cacatgcgtc ctacctgtga     840
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 279
58 <212> TYPE: PRT
59 <213> ORGANISM: Homo sapiens
61 <400> SEQUENCE: 2
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64 1               5                   10                  15
67 Ser Val Gly Leu Ser Glu Gly Pro Ala Gly Ser Arg Ser Gly Arg Leu
68              20                  25                  30
71 Phe Arg Pro Pro Ser Pro Ala Pro Ala Ala Pro Gly Ala Arg Leu Leu
72          35                  40                  45
75 Arg Leu Pro Gly Ser Gly Ala Val Gln Ala Ala Ser Pro Glu Arg Ala
76      50                  55                  60
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 79 Gly Tyr Thr Glu Ala Leu Arg Ala Ala Val Ala Glu Leu Arg Ala Gly
 80 65                  70              75                  80
 83 Ala Val Val Ala Val Pro Thr Asp Thr Leu Tyr Gly Leu Ala Cys Ala
 84              85                  90                  95
 87 Ala Ser Cys Ser Ala Ala Leu Arg Ala Val Tyr Arg Leu Lys Gly Arg
 88              100             105             110
 91 Ser Glu Ala Lys Pro Leu Ala Val Cys Leu Gly Arg Val Ala Asp Val
 92          115             120             125
 95 Tyr Arg Tyr Cys Arg Val Arg Val Pro Glu Gly Leu Leu Lys Asp Leu
 96      130             135             140
 99 Leu Pro Gly Pro Val Thr Leu Val Met Glu Arg Ser Glu Glu Leu Asn
100 145             150             155                 160
103 Lys Asp Leu Asn Pro Phe Thr Pro Leu Val Gly Ile Arg Ile Pro Asp
104              165             170             175
107 His Ala Phe Met Gln Asp Leu Ala Gln Met Phe Glu Gly Pro Leu Ala
108          180             185             190
111 Leu Thr Ser Ala Asn Leu Ser Ser Gln Ala Ser Ser Leu Asn Val Glu
112          195             200             205
115 Glu Phe Gln Asp Leu Tyr Pro Gln Leu Ser Leu Val Ile Asp Gly Gly
116      210             215             220
119 Gln Ile Gly Asp Gly Gln Ser Pro Glu Cys Arg Leu Gly Ser Thr Val
120 225             230             235             240
123 Val Asp Leu Ser Val Pro Gly Lys Phe Gly Ile Ile Arg Pro Gly Cys
124              245             250             255
127 Ala Leu Glu Ser Thr Thr Ala Ile Leu Gln Gln Lys Tyr Gly Leu Leu
128          260             265             270
131 Pro Ser His Ala Ser Tyr Leu
132          275
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 1387
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
140 <220> FEATURE:
141 <221> NAME/KEY: misc_feature
142 <222> LOCATION: (1)..(1387)
143 <223> OTHER INFORMATION: The letter "n" stands for a substitution base.
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149 cttgtaggca ttcggattcc tgatcatgct tttatgcaag acttggctca gatgtttgag    120
151 ggtccgcttg ctctcactag tgccaacctc agctcccagg ccagttctct gaatgtcgag    180
153 gagttccagg atctctggcc tcagttgtcc ttggttattg atgggggaca aattgggggat    240
155 ggccagagcc ccgagtgtcg ccttggctca actgtggttg atttgtctgt gcccggaaag    300
157 tttggcatca ttcgtccagg gtgtgcctgg gaaagtacta cagccatcct ccaacagaag    360
159 tacggactgc tcccctcaca tgcgtcctac ctgtgaaact ctgggaagca ggaaggccca    420
161 agacctggtg ctggatacta tgtgtctgtc cactgacgac tgtcaaggcc tcatttgcag    480
163 aggccaccgg agctagggca ctagcctgac tttttaaggca gtgtgtcttt ctgagcactg    540
165 tagaccaagc ccttggagct gctggtttag ccttgcacct ggggaaagga tgtatttatt    600
167 tgtattttca tatatcagcc aaaagctgaa tggaaaagtt aagaacattc ctaggtggcc    660
169 ttattctaat aagtttcttc tgtctgtttt gttttttcaat tgaaaagtaa ttaaataaca    720
```
W--> 147

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W--> 171 gatttagaat ctagtgagag cntcctctct gggggtggtg gcatttaagg ttcaacccan    780
W--> 173 ccnagaagtg ctgcgctgtt taaaaagtct caggtggctg cgtgtggtgg ctcatgcctg    840
     175 taatcccaac attctgggag gcccaggcgg gagaactgct tgagcccagg agttcagaat    900
     177 cagcctgggc aacatagcaa tactccgtct cataaaaatt aataaataaa aagtctcagg    960
     179 tgaccaaagg ctcctgaagc tagaaccagg tttggataaa gattgaagag ccacaggcca   1020
     181 ctcttccctc tgagccattg ggcctagtgg tgtcatgtat tgtaattgct cgcagggaga   1080
     183 gcagtctttt tggtgtaata gtgggatgtc tgcttagttg gcaggggttc agtccaaatg   1140
W--> 185 gaagaatatt gggaaataaa cctccnctat cctttatagc cagggacttt tttcttattt   1200
     187 attcataaaa taaattatag ttaattatac ccataacacc tttatttaaa tccagtgttc   1260
     189 tccgcagcct tttgtctatt tatatgtgta ccaagtgtta aacataatta ttattgggca   1320
W--> 191 tttgaacntg tttttcntta naganatnct gnnattaaac atatttgtna atggnaaaaa   1380
     193 aaaaaaa                                                           1387
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     197 <211> LENGTH: 930
     198 <212> TYPE: DNA
     199 <213> ORGANISM: Mus musculus
     201 <400> SEQUENCE: 4
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     204 agcgacgggc cggctagttc tggccgcggc tgccgcctcc tactccctcc tgagcccgct    120
     206 ccggcgctgc cggggggcccg gctgctgcgg cttccggaga gcgagcccgt ggaagccgcg    180
     208 agccccgagc gcgccggctg gaccgaggcg ctgcgggccg ccgtggccga gctgcgcgcc    240
     210 ggcgccgtgg tggcggtccc gaccgacacg ctctacggcc tggcctgctc ggcgagcagc    300
     212 tcggcggccc tgagttgcgt gtaccgcctc aaaggccgca gcgaggccaa gccgctggcc    360
     214 gtgtgcctgg gccgcgtggc cgacgtctac aggtactgtc aggtgagagt acctagggag    420
     216 ctcctggaag acctgttccc aggccctgtg accctggtga tggagcgctc cgaggagctc    480
     218 aacaaagacc tgaacccctt tactcgtctt gttggcatcc ggattcctga ccatgccttc    540
     220 atgctggact tggcccagat gtttgggggga ccacttgcac tcactagtgc caacctcagc    600
     222 tcccaggcca gttctctgag tgttgaggag ttccaagacc tctggcctca tttgtccctt    660
     224 gtcattgatg ggggggccaat tggggatagt cagagccctg agtgtcgcct cggctctact    720
     226 gtggttgact tatctgtgcc tggaaagttt ggcattattc gcccaggctg tgccctggaa    780
     228 aacactacat cgatcctcca gcagaaatat gggctgctcc cttcacaggg gtcctgttca    840
     230 tgaaacttgg gaggacccaa ggacatgctg gatactatgt gtctgctact ggatgcaaag    900
     232 cctcattgcc tgaggttcct acatctatag                                    930
     235 <210> SEQ ID NO: 5
     236 <211> LENGTH: 280
     237 <212> TYPE: PRT
     238 <213> ORGANISM: Mus musculus
     240 <400> SEQUENCE: 5
     242 Met Ser Thr Ala Arg Pro Cys Ala Gly Leu Arg Ala Ala Val Ala Ala
     243 1               5                   10                  15
     246 Gly Met Gly Leu Ser Asp Gly Pro Ala Ser Ser Gly Arg Gly Cys Arg
     247             20                  25                  30
     250 Leu Leu Leu Pro Pro Glu Pro Ala Pro Ala Leu Pro Gly Ala Arg Leu
     251         35                  40                  45
     254 Leu Arg Leu Pro Glu Ser Glu Pro Val Glu Ala Ala Ser Pro Glu Arg
     255     50                  55                  60
     258 Ala Gly Tyr Thr Glu Ala Leu Arg Ala Ala Val Ala Glu Leu Arg Ala
     259 65                  70                  75                  80
     262 Gly Ala Val Val Ala Val Pro Thr Asp Thr Leu Tyr Gly Leu Ala Cys
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Input Set : A:\266_171.ST25.txt
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263                    85              90              95
266 Ser Ala Ser Ser Ser Ala Ala Leu Ser Cys Val Tyr Arg Leu Lys Gly
267              100            105            110
270 Arg Ser Glu Ala Lys Pro Leu Ala Val Cys Leu Gly Arg Val Ala Asp
271         115            120            125
274 Val Tyr Arg Tyr Cys Gln Val Arg Val Pro Arg Glu Leu Leu Glu Asp
275     130            135            140
278 Leu Phe Pro Gly Pro Val Thr Leu Val Met Glu Arg Ser Glu Glu Leu
279 145            150            155                 160
282 Asn Lys Asp Leu Asn Pro Phe Thr Arg Leu Val Gly Ile Arg Ile Pro
283            165            170            175
286 Asp His Ala Phe Met Leu Asp Leu Ala Gln Met Phe Gly Gly Pro Leu
287            180            185            190
290 Ala Leu Thr Ser Ala Asn Leu Ser Ser Gln Ala Ser Ser Leu Ser Val
291         195            200            205
294 Glu Glu Phe Gln Asp Leu Tyr Pro His Leu Ser Leu Val Ile Asp Gly
295     210            215            220
298 Gly Pro Ile Gly Asp Ser Gln Ser Pro Glu Cys Arg Leu Gly Ser Thr
299 225            230            235                 240
302 Val Val Asp Leu Ser Val Pro Gly Lys Phe Gly Ile Ile Arg Pro Gly
303            245            250            255
306 Cys Ala Leu Glu Asn Thr Thr Ser Ile Leu Gln Gln Lys Tyr Gly Leu
307         260            265            270
310 Leu Pro Ser Gln Gly Ser Cys Ser
311      275            280
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314 <210> SEQ ID NO: 6
315 <211> LENGTH: 702
316 <212> TYPE: DNA
317 <213> ORGANISM: Bos taurus
319 <400> SEQUENCE: 6
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322 gggcgccgtg taccgtgtca agggccgcag cgagaccaag ccgctggccg tatgcctggg    120
324 ccgcgtggcc gacgtctaca ggtactgcca cgtgagagta cctgaggggc tcctgaagga    180
326 cctgttgcca ggaccagtga ccctggtgat ggaacgctca gaggagctca acaaggacct    240
328 gaatcctttc actcctcttg taggcatccg gattcctgac cacgccttca tgcaggactt    300
330 ggtccagatg tttgggggc cactcgctct caccagtgcc aacctcagct cccagtccag     360
332 ctctctgaat gttgaggaat tccaggacct gtggcctcac ttgtccctga tcattggtgg    420
334 gggaccaatt ggggacggcc agagcccaga gtgtcgacta ggctcaactg tggttgactt    480
336 gtctgtgcct ggaaagtttg gcatcattcg tcctggttgt gcccttgaaa gtacttcagc    540
338 catcctccag gagtatgggc tgctcccctc acatggatcc tgctggtgac actctggagg    600
340 agggaaggcc caagggctgg tgctggacac tatgtgtccg actgctggtg gttggcaagg    660
342 cctcatttgc agaggctgct agggctacag tgttagtagt ct                       702
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345 <210> SEQ ID NO: 7
346 <211> LENGTH: 126
347 <212> TYPE: PRT
348 <213> ORGANISM: Bos taurus
350 <400> SEQUENCE: 7
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352 Met Glu Arg Ser Glu Glu Leu Asn Lys Asp Leu Asn Pro Phe Thr Pro
353 1              5              10             15
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356 Leu Val Gly Ile Arg Ile Pro Asp His Ala Phe Met Gln Asp Leu Val
357             20              25              30
360 Gln Met Phe Gly Gly Pro Leu Ala Leu Thr Ser Ala Asn Leu Ser Ser
361         35              40              45
364 Gln Ser Ser Ser Leu Asn Val Glu Glu Phe Gln Asp Leu Trp Pro His
365     50              55              60
368 Leu Ser Leu Ile Ile Gly Gly Gly Pro Ile Gly Asp Gly Gln Ser Pro
369 65              70              75              80
372 Glu Cys Arg Leu Gly Ser Thr Val Val Asp Leu Ser Val Pro Gly Lys
373             85              90              95
376 Phe Gly Ile Ile Arg Pro Gly Cys Ala Leu Glu Ser Thr Ser Ala Ile
377             100             105             110
380 Leu Gln Glu Tyr Gly Leu Leu Pro Ser His Gly Ser Cys Trp
381         115             120             125
384 <210> SEQ ID NO: 8
385 <211> LENGTH: 841
386 <212> TYPE: DNA
387 <213> ORGANISM: Rattus novartis
389 <220> FEATURE:
390 <221> NAME/KEY: misc_feature
391 <222> LOCATION: (491)..(491)
392 <223> OTHER INFORMATION: The letter "z" stands for sequence hybridizing.
395 <400> SEQUENCE: 8
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398 aagtttggca ttattcgctc aggctgtgcc ctggaaaata ctacagccat cctccagggg   120
400 aaatatgggc tgctcccttc acaggggtcc tgttcatgaa acttgggagg acccaagaac   180
402 catgctggat actatgtgtc tactacaggt tggcaaagcc tcattggctg aggttcctgg   240
404 agctacatct gtagcctagc tttttaggca gtgtccttgg ctctgaatcc tgtaggccag   300
406 ccagaagctt cgggttgagc cttgcaccca ggggaaggtt atatttactc tgtagattca   360
408 tgtgtcaacc cagaatggag ggaagaacat tcttagagtg accttattat tttaagtgcc   420
410 cctctcaccc caaccctgcc tataagttaa gtaacttgac tgcagaatta gaatgcatta   480
412 agagctgctt actggtgaac agtgaaattt ggtttaaaac cagccagaag cactaatgca   540
414 gtctagaagt ctcaggacca atgcagcaaa gtctaggagc cctggccaga gctttctggg   600
416 tacaggagag tggtcatttg gagaaaatta ttctaggagt tccaaatgaa ataatattga   660
418 aaataaaat cttgactgtt ttcagccagt gactttctta tttattggta tagttctctg    720
420 tttaattat ttaactcaga agtcatcttt gttcatatgt ctacctggta tttacataat    780
422 tatttttaag tatttgaact gtatttcttt attaaatatt tcttctacaa aaaaaaaaa    840
424 a                                                                  841
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/960,631A

DATE: 03/29/2002
TIME: 13:28:16

Input Set : **A:\266_171.ST25.txt**
Output Set: **N:\CRF3\03292002\I960631A.raw**

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L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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